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In the Claims

Please amend the claims by replacing all prior versions of the claims pursuant to 37 C.F.R. §1.121 as modified by 68 Fed. Reg. 38611 (June 30, 2003) as indicated below.

1. (Currently Amended) A method of modifying the content or composition, or content and composition, of a metabolite in the ~~storage organ~~ seed of a plant ~~, said metabolite selected from the group consisting of fatty acid, starch, soluble non-starch polysaccharide, insoluble non-starch polysaccharide, fibre, and total protein nitrogen, said method~~ comprising:

(i) expressing in the ~~storage organ~~ seed of the plant a chimeric gene comprising a nucleotide sequence encoding a sulfur-rich protein placed operably in connection with a promoter sequence capable of conferring expression in ~~said storage organ~~ the seed, wherein the sulfur-rich protein is a 2S protein or the Asp1 synthetic protein;

(ii) determining the content or composition, or content and composition, of a metabolite in ~~said storage organ~~ the seed, said metabolite selected from the group consisting of fatty acid, starch, soluble non-starch polysaccharide, insoluble non-starch polysaccharide, fibre and total protein nitrogen, and

(iii) selecting a plant having a modified content or composition, or content and composition, of ~~said~~ a metabolite in the ~~storage organ~~ seed thereof, as compared to a plant in which said chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley,

rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea, and

wherein the modified content or composition, or content and composition, of a metabolite in the seed of a plant is at least one of:

a) increased total protein nitrogen content;
b) decreased total starch content;
c) increased or decreased fatty acid content;
d) modified fatty acid composition;
e) increased or decreased fibre content; or
f) modified fibre composition.

2-4. (Canceled)

5. (Previously presented) The method according to claim 1 wherein the total protein nitrogen content is increased.

6. (Previously presented) The method according to claim 1 wherein the fibre content or composition is modified.

7. (Canceled)

8. (Previously presented) The method according to claim 1 wherein the fatty acid content is increased or decreased.

9-10. (Canceled)

11. (Previously presented) The method according to claim 1 wherein the sulfur-rich protein is Brazil Nut Protein (BNP).

12. (Previously presented) The method according to claim 1 wherein the sulfur-rich protein is sunflower seed albumin (SSA).

13. (Previously presented) The method according to claim 1 wherein the sulfur-rich protein is the Asp1 synthetic protein.

14. (Previously presented) The method according to claim 1 wherein the plant is a dicotyledonous plant.

15. (Previously presented) The method according to claim 14 wherein the dicotyledonous plant is a pea or chickpea plant.

16. (Previously presented) The method according to claim 1 wherein the promoter sequence comprises the pea vicilin gene promoter sequence.

17. (Previously presented) The method according to claim 1 wherein the plant is a monocotyledonous plant.

18. (Original) The method according to claim 17 wherein the monocotyledonous plant is a rice plant.

19. (Previously presented) The method according to claim 1 wherein the promoter comprises a *Triticum aestivum* HMW glutenin promoter sequence.

20. (Previously presented) The method according to claim 1 further comprising the first steps of:

(i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and

(ii) regenerating an intact plant therefrom.

21. (Currently Amended) A method of increasing the total protein nitrogen content of seeds of a plant, said method comprising

(i) expressing in the seeds of the plant a chimeric gene comprising a nucleotide sequence encoding a sulfur-rich protein placed operably in connection with a promoter sequence capable of conferring expression in said seeds, wherein the sulfur-rich protein is a 2S protein or the Asp1 synthetic protein, said nucleotide sequence also positioned upstream of a transcription termination sequence;

(ii) determining the ~~level~~ content of total protein nitrogen in the seeds; and

~~(ii)~~(iii) selecting a plant having an increased total protein nitrogen content in the seeds thereof as compared to the seeds of a plant which does not express the chimeric gene,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

22. (Original) The method according to claim 21 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

23. (Original) The method according to claim 21 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

24. (Previously presented) The method according to claim 22 wherein the plant is pea or chickpea.

25. (Original) The method according to claim 21 wherein the promoter sequence is a wheat HMW glutenin gene promoter and the plant is a monocotyledonous plant.

26. (Original) The method according to claim 21 wherein the chimeric gene further comprises the wheat HMW glutenin gene promoter and/or NOS transcription terminator sequences.

27. (Previously presented) The method according to claim 25 wherein the plant is a rice plant.

28. (Currently Amended) A method of ~~modifying the~~ increasing or decreasing fatty acid content of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds:

(ii) determining the ~~level~~ content of a fatty acid in the seed; and

(iii) selecting a plant having ~~a modified~~ increased or decreased content of the fatty acid ~~content~~ in the seeds thereof as compared to the seeds of a plant which does not express the chimeric gene,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

29. (Original) The method according to claim 28 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

30. (Original) The method according to claim 28 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

31. (Canceled)

32. (Previously presented) The method according to claim 29 wherein if the plant is pea the ~~level~~ content of fatty acids in the seeds is decreased.

33. (Currently Amended) A method of modifying the fatty acid composition of seeds of a plant, said method comprising

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant;

(ii) determining the fatty acid composition of the seeds; and

(iii) selecting a plant having a modified fatty acid composition in the seeds thereof, as compared to seeds of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

34. (Original) The method according to claim 33 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

35. (Original) The method according to claim 33 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

36. (Canceled)

37. (Previously presented) The method according to claim 33 wherein the fatty acid is selected from the group consisting of: myristic acid, stearic acid, gadoleic acid, behenic acid, lignoceric acid, oleic acid, linoleic acid, linolenic acid and erucic acid.

38. (Currently Amended) A method of decreasing the starch content of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed

upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant:

(ii) determining the starch content of the seeds; and

(iii) selecting a plant having a decreased starch content in the seeds thereof, as compared with seeds of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

39. (Original) The method according to claim 38 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

40. (Original) The method according to claim 38 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

41. (Previously presented) The method according to claim 39 wherein the plant is a pea plant.

42. (Currently Amended) A method of modifying the amino acid composition of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression

on said structural gene in the seeds of said plant;

(ii) determining the amino acid composition of the seeds; and

(iii) selecting a plant having a modified amino acid composition in the seeds thereof, as compared to a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

43. (Original) The method according to claim 42 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

44. (Original) The method according to claim 42 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

45. (Previously presented) The method according to claim 43 wherein the plant is pea or chickpea.

46. (Original) The method according to claim 45 wherein the. proportion of arginine relative to other amino acids is increased.

47. (Currently Amended) A method of ~~modifying~~ increasing or decreasing the fibre content of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence

encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant;

(ii) determining the fibre content of the seeds; and

(iii) selecting a plant having ~~a modified~~ an increased or a decreased content of fibre ~~content~~ in the seeds thereof, as compared with seeds of a plant which does not express said chimeric gene,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

48. (Original) The method according to claim 47 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

49. (Original) The method according to claim 47 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

50. (Canceled)

51. (Previously presented) The method according to claim 48 wherein if the plant is a pea plant the ~~level~~ content of fibre in the seed is increased.

52. (Currently Amended) A method of modifying the fibre ~~quality~~ composition of seeds of a plant, said method comprising:

(i) the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant;

(ii) determining the fibre ~~quality~~ composition of the seeds; and

(iii) selecting a plant having a modified fibre ~~quality~~ composition in the seeds thereof, as compared with seeds of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

53. (Original) The method according to claim 52 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

54. (Original) The method according to claim 53 wherein the chimeric gene further comprises the pea vicilin gene promoter and transcription terminator sequences.

55. (Canceled)

56. (Currently Amended) The method according to claim 52 wherein the ~~level~~ content of soluble ~~NSP and/or~~ non-starch polysaccharide, or the ~~level~~ content of insoluble ~~NSP~~ non-starch polysaccharide, or the content of both in

the seed is decreased.

57. (Currently Amended) The method according to claim 52 wherein the ~~level~~ content of lignin in the seed is increased.

58-63. (Canceled)

64. (Currently Amended) The method according to any one of claims ~~1,~~ 21, 28, 33, 38, 42, 47, or 52 further comprising the first steps of:

(i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and

(ii) regenerating an intact plant therefrom.

65. (Currently Amended) A transformed plant ~~produced~~ having a modified content or composition, or content and composition, of a metabolite in its seed, wherein the modification is by the method according to any one of claims 1, 21, 28, 33, 38, 42, 47, 52; or 102, or progeny of said plant, wherein said progeny comprises at least one copy of the chimeric gene in an expressible format ~~, said plant being wheat, oats, maize, barley, rice, sorghum, millet, oilseed rape, rye, safflower, sunflower, potato, sweet potato, beetroot, taro, Jerusalem artichoke, onion, garlic, soybean, pea, bean (including joba and common bean), lentil, chickpea or sugar cane~~.

66. (Canceled)

67. (Previously presented) A ~~plant part~~ seed derived from the plant according to claim 65 wherein said ~~plant part~~ seed comprises at least one copy of the chimeric gene ~~present in said plant or progeny~~ in an expressible format.

68. (Canceled)

69. (Original) The ~~plant part according to claim 67 consisting of seeds~~ seed derived from the transformed plant of claim 65, wherein the seed has a modified content or composition, or content and composition of a metabolite, wherein the modification is at least one of:

a) increased total protein nitrogen content;
b) decreased total starch content;
c) increased or decreased fatty acid content;
d) modified fatty acid composition;
e) increased or decreased fibre content; or
f) modified fibre composition.

70-87. (Canceled)

88. (Currently Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) ~~and wherein the storage organ is a seed~~ and wherein the total protein nitrogen content of the seed is increased.

89. (Currently Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) ~~and wherein the storage organ is a seed~~ and wherein the amino acid composition of the seed is modified.

90. (Currently Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) ~~and wherein the storage organ is a seed~~ and wherein expression of the chimeric gene in the seed increases or decreases the fibre content of the seed.

91. (Currently Amended) The method of claim 1 or claim 102 wherein the chimeric gene encodes sunflower seed albumin (SSA) ~~and wherein the storage organ is a seed~~ and wherein expression of the chimeric gene in the seed modifies the fibre composition of the seed.

92. (Currently Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) ~~and wherein the storage organ is a seed~~ and wherein expression of the chimeric gene in the seed decreases the total starch content of the seed.

93. (Currently Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) ~~and wherein the storage organ is a seed~~ and wherein expression of the chimeric gene in the seed increases or decreases the total fatty acid content of the seed.

94. (Currently Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) ~~and wherein the storage organ is a seed~~ and wherein expression of the chimeric gene in the seed modifies the fatty acid composition of the seed.

95. (Canceled)

96. (Previously presented) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and further comprises a promoter sequence which confers strong expression at least in the seeds of the plant.

97. (Previously presented) The method according to claim 96 wherein the promoter is the pea vicilin promoter.

98. (Previously presented) The method according to claim 96 wherein the promoter is the wheat HMW glutenin promoter.

99. (Previously presented) The method of claim 96 wherein the chimeric gene further comprises a transcription terminator sequence placed downstream of the sequence encoding SSA.

100. (Previously presented) The method of claim 99 wherein the transcription terminator sequence is the pea vicilin gene terminator sequence.

101. (Currently Amended) The method according to claim 1 or claim 102, wherein the content or composition, or content and composition, of more than one metabolite in the ~~storage organ~~ seed of the plant is modified ~~, and wherein at least one of said metabolites is selected from the group consisting of fatty acid, starch, soluble non-starch polysaccharide, insoluble non-starch polysaccharide, fibre and total protein nitrogen~~.

102. (Currently Amended) A method of modifying the content or composition, or content and composition, of a metabolite in the ~~storage organ~~ seed of a plant ~~, said metabolite selected from the group consisting of fatty acid, starch, soluble non-starch polysaccharide, insoluble non-starch polysaccharide, fibre, and total protein nitrogen, said method~~ comprising:

(i) expressing in the ~~storage organ~~ seed of the plant a chimeric gene comprising a nucleotide sequence encoding a sulfur-rich protein placed operably in connection with a promoter sequence capable of conferring expression in ~~said storage organ~~ the seed, wherein the sulfur-rich protein is a 2S protein or the Aspl synthetic protein; and

(ii) determining whether the content or composition, or content and composition, of a metabolite in ~~said storage organ~~ the seed of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed ~~, said metabolite selected from the group consisting of fatty acid, starch, soluble non-starch polysaccharide, insoluble non-starch polysaccharide, fibre and total protein nitrogen~~

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea, and

wherein the modified content or composition, or content and composition, of a metabolite in the seed of a plant is at least one of:

a) increased total protein nitrogen content;

b) decreased total starch content;

c) increased or decreased fatty acid content;

d) modified fatty acid composition;

e) increasing or decreasing fibre content; or

f) modified fibre composition.

103. (Currently Amended) A method of increasing the total protein nitrogen content of seeds of a plant, said method comprising:

(i) expressing in the seeds of the plant a chimeric gene comprising a nucleotide sequence encoding a sulfur-rich protein placed operably in connection with a promoter sequence capable of conferring expression in said seeds, wherein the sulfur rich protein is a 2S protein or the Aspl synthetic protein, said nucleotide sequence also positioned upstream of a transcription termination sequence; and

(ii) determining whether the ~~level~~ content of total protein nitrogen in the seeds of ~~said plants~~ the plant is increased as compared to that of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

104. (Currently Amended) A method of ~~modifying~~ increasing or decreasing the fatty acid content of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence

capable of conferring expression on said structural gene in the seeds; and

(ii) determining ~~the level~~ whether the content of a fatty acid in the seeds of the plant is increased or decreased as compared to that of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

105. (Currently Amended) A method of modifying the fatty acid composition of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and

(ii) determining whether the fatty acid composition of the seeds of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

106. (Currently Amended) A method of decreasing the starch content of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence

encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and

(ii) determining whether the starch content of the seeds of the plant is decreased as compared to that of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

107. (Currently Amended) A method of modifying the amino acid composition of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and

(ii) determining whether the amino acid composition of the seeds of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

108. (Currently Amended) A method of ~~modifying~~ increasing or decreasing the fibre content of seeds of a plant, said method

comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and

(ii) determining whether the fibre content of the seeds of the plant is increased or decreased as compared to that of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

109. (Currently Amended) A method of modifying the fibre ~~quality~~ composition of seeds of a plant, said method comprising:

(i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and

(ii) determining whether the fibre ~~quality~~ composition of the seeds of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed,

wherein the plant is wheat, oats, maize, barley,

rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

110. (Currently Amended) The method according to claim 1, wherein the total protein nitrogen content of ~~storage organ~~ the seed of the plant is increased by at least 10%.

111. (Canceled)

112. (Currently Amended) The method according to claim 1, wherein the total fibre content of the ~~storage organ~~ seed of the plant is increased or decreased by at least 5%.

113. (Currently Amended) The method according to claim 1, wherein the total starch content of ~~storage organ~~ the seed of the plant is reduced by at least 10%.

114. (Currently Amended) The method according to claim 1. wherein the total fatty acid content of ~~storage organ~~ the seed of the plant is increased or decreased by at least 5%.

115. (Currently Amended) The method according to claim 1, wherein the content of any one fatty acid in the ~~storage organ~~ seed of the plant is increased or decreased by at least 5%.